

IN THE CLAIMS

1-3. (canceled) .

4. (currently amended) A method for ~~reducing sequencing errors by~~ sequencing, ~~recovering and resequencing a single-stranded template~~ nucleic acid, the method comprising:
- (a) forming an array of immobilised single-stranded template nucleic acid molecules wherein the density of immobilised single-stranded template nucleic acid molecules is 10^6 - 10^9 different template sequences per cm^2 ;
 - (b) determining the sequences of the immobilised single-stranded template nucleic acid molecules by synthesising a complementary copy of the template sequences, thereby performing a first round of sequencing;
 - (c) removing the complementary copy of the template sequence ~~synthetic strand~~; and
 - (d) performing a second round of sequencing of the immobilised single-stranded template nucleic acid molecules, and wherein comparison of
 - (e) comparing the first and second rounds of sequencing of each immobilized single-stranded template nucleic acid molecule to confirm sequencing data ~~reduces sequencing errors.~~

5-26. (canceled).

27. (currently amended) The method of claim 4, wherein the template nucleic acid molecules ~~polynucleotides~~ are attached to a double stranded anchor.

- 28 (currently amended) The method of claim 27 28, wherein the double stranded anchor comprises a self complementary hairpin.

- 29 (previously presented) The method of claim 27, wherein the double stranded anchor comprises a recognition site for a restriction endonuclease.
- 30 (previously presented) The method of claim 4, wherein the 10^6 - 10^9 templates are individually resolvable single molecules.
- 31 (previously presented) The method of claim 4, wherein the sequencing determination is carried out using cycles of incorporation and detection of fluorescently labeled nucleotides.
- 32 (previously presented) The method of claim 31, wherein the fluorescent nucleotides are detected using a microscope with total internal reflection based imaging.
33. (new) The method of claim 4, wherein said synthesizing a complementary copy of the template sequences comprises employing a polymerase enzyme to synthesize a complementary strand on the template strand one base at a time.